BLAST 2 SEQUENCES

This functionality is now available in the main BLAST pages and this link will be removed in the near future. Step-by-step **instructions** for use are available.

This tool produces the alignment of two given sequences using BLAST engine for local alignment.
The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site
Reference: Tatiana A. Tatusova, Thomas L. Madden (1999), "Blast 2 sequences - a new tool for comparing protein and nucleotide sequences", FEMS Microbiol Lett. 174:247-250

Program `blastn` Matrix `Not Applicable`

Parameters used in BLASTN program only:
Reward for a match: `1`   Penalty for a mismatch: `-2`

☐ Use Mega BLAST Strand option `Both strands`   View option `Standard`
Masking character option `X for protein, n for nucleotide`   Masking color option `Black`
☐ Show CDS translation

Open gap `5` and extension gap `2` penalties
gap x_dropoff `50` expect `10.0` word size `11` Filter ☑ `Align`

Sequence 1
Enter accession, GI or sequence in FASTA format from: `0`   to: `0`

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtggtgtca
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga
gaaatctttg gtgttttcgc ttttggcact caaaagtatg tccagaaaat
cccagcgcct tttctgagta gtatcttgtt ttagcttatc cttaagagac
tccttccggt cctggattac tttctctgtg aactgatgaa gttcttggtt
aaatttagaa aagatttggc cttgagagct gaatttgaaa accaggtcgt
```

or upload FASTA file `_____` `Browse...`

Sequence 2
Enter accession, GI or sequence in FASTA format from: `0`   to: `0`

```
H21976
```

or upload FASTA file `_____` `Browse...`
`Align` `Clear Input`

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

Blast 2 Sequences results

NCBI

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2
x_dropoff: 0   expects: 10.000   wordsize: 11   Filter ☑   View option Standard
Masking character option X for protein, n for nucleotide   Masking color option Black
☐ Show CDS translation   Align

Sequence 1: lcl|1
Length = 379

Sequence 2: gi|890671|yl38c11.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:160532 5' similar to
SP:CP4B_RABIT P15128 CYTOCHROME P450 IVB1 ;, mRNA sequence.
Length = 332

No significant similarity was found

```
CPU time:     0.04 user secs.      0.04 sys. secs      0.08 total secs.
```

BLAST 2 SEQUENCES

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Program `blastn ▾` Matrix `Not Applicable ▾`

Parameters used in BLASTN program only:
Reward for a match: `1`   Penalty for a mismatch: `-2`

☐ Use Mega BLAST   Strand option `Both strands ▾`   View option `Standard ▾`
Masking character option `X for protein, n for nucleotide ▾`   Masking color option `Black ▾`
☐ Show CDS translation

Open gap `5` and extension gap `2` penalties
gap x_dropoff `50` expect `10.0` word size `11` Filter ☑ `Align`

Sequence 1
Enter accession, GI or sequence in FASTA format from: `0` to: `0`

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtggtgtca
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga
gaaatctttg gtgttttcgc ttttggcact caaaagtatg tccagaaaat
cccagcgcct tttctgagta gtatcttgtt ttagcttatc cttaagagac
tccttccggt cctggattac tttctctgtg aactgatgaa gttcttggtt
aaatttagaa aagatttggc cttgagagct gaatttgaaa accaggtcgt
```

or upload FASTA file `_____` `Browse...`

Sequence 2
Enter accession, GI or sequence in FASTA format from: `0` to: `0`

```
H21977
```

or upload FASTA file `_____` `Browse...`
`Align` `Clear Input`

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2
x_dropoff: 0   expect: 10.000   wordsize: 11   Filter ☑   View option Standard
Masking character option X for protein, n for nucleotide   Masking color option Black
☐ Show CDS translation   Align

Sequence 1: lcl|1
Length = 379

Sequence 2: gi|890672|yl38c11.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:160532 3', mRNA sequence.
Length = 444

No significant similarity was found

CPU time: 0.03 user secs.   0.01 sys. secs   0.04 total secs.

BLAST 2 SEQUENCES

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The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site
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Program `blastn` Matrix `Not Applicable`

Parameters used in BLASTN program only:
Reward for a match: `1`   Penalty for a mismatch: `-2`

☐ Use Mega BLAST   Strand option `Both strands`   View option `Standard`
Masking character option `X for protein, n for nucleotide`   Masking color option `Black`
☐ Show CDS translation

Open gap `5`   and extension gap `2`   penalties
gap x_dropoff `50`   expect `10.0`   word size `11`   Filter ☑ `Align`

Sequence 1
Enter accession, GI or sequence in FASTA format from: `0`   to: `0`

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtggtgtca
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga
gaaatctttg gtgttttcgc ttttggcact caaaagtatg tccagaaaat
cccagcgcct tttctgagta gtatcttgtt ttagcttatc cttaagagac
tccttccggt cctggattac tttctctgtg aactgatgaa gttcttggtt
aaatttagaa aagatttggc cttgagagct gaatttgaaa accaggtcgt
```

or upload FASTA file `                    ` `Browse...`

Sequence 2
Enter accession, GI or sequence in FASTA format from: `0`   to: `0`

```
H25577
```

or upload FASTA file `                    ` `Browse...`
`Align` `Clear Input`

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Blast 2 Sequences results

NCBI

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2
x_dropoff: 0   expects: 10.000   wordsize: 11   Filter ☑   View option Standard
Masking character option X for protein, n for nucleotide   Masking color option Black
☐ Show CDS translation   Align

Sequence 1: lcl|1
Length = 379

Sequence 2: gi|894700|yl48g04.s1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:161526 3', mRNA sequence.
Length = 421

No significant similarity was found

CPU time: 0.04 user secs.   0.03 sys. secs   0.07 total secs.

BLAST 2 SEQUENCES

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The stand-alone executable for blasting two sequences (bl2seq) can be retrieved from NCBI ftp site
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Program `blastn` ▾ Matrix `Not Applicable` ▾

Parameters used in BLASTN program only:
Reward for a match: `1`   Penalty for a mismatch: `-2`

☐ Use Mega BLAST Strand option `Both strands` ▾   View option `Standard` ▾
Masking character option `X for protein, n for nucleotide` ▾   Masking color option `Black` ▾
☐ Show CDS translation

Open gap `5`   and extension gap `2`   penalties
gap x_dropoff `50`   expect `10.0`   word size `11`   Filter ☑ `Align`

Sequence 1
Enter accession, GI or sequence in FASTA format from: `0`   to: `0`

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtggtgtca
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga
gaaatctttg gtgttttcgc ttttggcact caaagtatg tccagaaaat
cccagcgcct tttctgagta gtatcttgtt ttagcttatc cttaagagac
tccttccggt cctggattac tttctctgtg aactgatgaa gttcttggtt
aaatttagaa aagatttggc cttgagagct gaatttgaaa accaggtcgt
```

or upload FASTA file ` ` `Browse...`

Sequence 2
Enter accession, GI or sequence in FASTA format from: `0`   to: `0`

```
H25624
```

or upload FASTA file ` ` `Browse...`
`Align` `Clear Input`

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

Blast 2 Sequences results

NCBI

PubMed   Entrez   BLAST   OMIM   Taxonomy   Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2
x_dropoff: 0   expect: 10.000   wordsize: 11   Filter ☑   View option | Standard |
Masking character option | X for protein, n for nucleotide | Masking color option | Black |
☐ Show CDS translation | Align |

Sequence 1: lcl|1
Length = 379

Sequence 2: gi|894747|yl48g04.r1 Soares breast 3NbHBst Homo sapiens cDNA clone IMAGE:161526 5' similar to gb:J02871 CYTOCHROME P450 IVB1 (HUMAN);contains Alu repetitive element;, mRNA sequence.
Length = 432

No significant similarity was found

CPU time: 0.04 user secs.   0.03 sys. secs   0.07 total secs.

NCBI   *Entrez*   *BLAST 2 sequences*   *BLAST*   *Example*   *Help*

BLAST 2 SEQUENCES

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Program `blastn ▼` Matrix `Not Applicable ▼`

Parameters used in BLASTN program only:
Reward for a match: `1`   Penalty for a mismatch: `-2`

☐ Use Mega BLAST   Strand option `Both strands ▼`   View option `Standard ▼`
Masking character option `X for protein, n for nucleotide ▼`   Masking color option `Black ▼`
☐ Show CDS translation

Open gap `5`   and extension gap `2`   penalties
gap x_dropoff `50`   expect `10.0`   word size `11`   Filter ☑ `Align`

Sequence 1
Enter accession, GI or sequence in FASTA format from: `0`   to: `0`

```
actttgccaa gcagtaaagg atccaggaga tagcactgga tgtggtgtca
tgtcctgcaa acatgaacgt tttcacttca gcctggagat ctgcttcaga
gaaatctttg gtgttttcgc ttttggcact caaaagtatg tccagaaaat
cccagcgcct tttctgagta gtatcttgtt ttagcttatc cttaagagac
tccttccggt cctggattac tttctcttgtg aactgatgaa gttcttggtt
aaatttagaa aagatttggc cttgagagct gaatttgaaa accaggtcgt
```

or upload FASTA file `              ` `Browse...`

Sequence 2
Enter accession, GI or sequence in FASTA format from: `0`   to: `0`

```
AA003705
```

or upload FASTA file `              ` `Browse...`
`Align` `Clear Input`

Comments and suggestions to blast-help@ncbi.nlm.nih.gov

Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTN 2.2.18 [Mar-02-2008]

Match: 1   Mismatch: -2   gap open: 5   gap extension: 2
x_dropoff: 0   expect: 10.000   wordsize: 11   Filter ☑ View option Standard
Masking character option X for protein, n for nucleotide   Masking color option Black
☐ Show CDS translation   Align

Sequence 1: lcl|1
Length = 379

Sequence 2: gi|1447205|mg61a02.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone
IMAGE:437450 5', mRNA sequence.
Length = 331

No significant similarity was found

CPU time: 0.02 user secs.   0.03 sys. secs   0.05 total secs.